RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/537,676
Source: PCT
Date Processed by STIC: 6-21-05

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/537,676 CRF Edit Date: 6/21/05
Edited by: TCR

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

__/__ Deleted: __/__ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

_____

___ Moved responses to same line as heading/numeric identifier, specifically:

_____

___ Other:

_____

_____

_____

Revised 09/09/2003

Raw Sequence Listing before editing,
for reference only

PCT

RAW SEQUENCE LISTING DATE: 06/21/2005
PATENT APPLICATION: **US/10/537,676** TIME: 13:38:24

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\06212005\J537676.raw**

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      3 <110> APPLICANT: Hinuma, Shuji
      4       MARUYAMA, Minoru
      5       FUJII, Ryo
      7 <120> TITLE OF INVENTION: Novel Use of EDG Receptor
      9 <130> FILE REFERENCE: 3127US0P
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/537,676
C--> 11 <141> CURRENT FILING DATE: 2005-06-06
     11 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/015836
     12 <151> PRIOR FILING DATE: 2003-12-11
     14 <150> PRIOR APPLICATION NUMBER: JP 2002-361415
     15 <151> PRIOR FILING DATE: 2002-12-12
     17 <160> NUMBER OF SEQ ID NOS: 45
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 364
     21 <212> TYPE: PRT
     22 <213> ORGANISM: human
     24 <400> SEQUENCE: 1
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     26                  5                  10                  15
     27 Thr Ala Met Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
     28              20                  25                  30
     29 Phe Tyr Asn Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val
     30          35                  40                  45
     31 Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met
     32      50                  55                  60
     33 Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
     34  65                  70                  75                  80
     35 His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
     36                  85                  90                  95
     37 Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
     38             100                 105                 110
     39 Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
     40         115                 120                 125
     41 Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
     42     130                 135                 140
     43 Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
     44 145                 150                 155                 160
     45 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
     46                 165                 170                 175
     47 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
     48             180                 185                 190
     49 Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
     50         195                 200                 205
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51 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
52     210                 215                 220
53 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
54 225                 230                 235                 240
55 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
56                 245                 250                 255
57 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr
58             260                 265                 270
59 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
60         275                 280                 285
61 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
62     290                 295                 300
63 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
64 305                 310                 315                 320
65 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly
66                 325                 330                 335
67 Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
68             340                 345                 350
69 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
70         355                 360
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 1092
74 <212> TYPE: DNA
75 <213> ORGANISM: human
77 <400> SEQUENCE: 2
78 atggctgcca tctctacttc catccctgta atttcacagc cccagttcac agccatgaat    60
79 gaaccacagt gcttctacaa cgagtccatt gccttctttt ataaccgaag tggaaagcat   120
80 cttgccacag aatggaacac agtcagcaag ctggtgatgg gacttggaat cactgtttgt   180
81 atcttcatca tgttggccaa cctattggtc atggtggcaa tctatgtcaa ccgccgcttc   240
82 cattttccta tttattacct aatggctaat ctggctgctg cagacttctt tgctgggttg   300
83 gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgttagcaca   360
84 tggctcctgc gtcagggcct cattgacacc agcctgacgg catctgtggc caacttactg   420
85 gctattgcaa tcgagaggca cattacggtt ttccgcatgc agctccacac acggatgagc   480
86 aaccggcggg tagtggtggt cattgtggtc atctggacta tggccatcgt tatgggtgct   540
87 atacccagtg tgggctggaa ctgtatctgt gatattgaaa attgttccaa catggcaccc   600
88 ctctacagtg actcttactt agtcttctgg gccatttca acttggtgac ctttgtggta   660
89 atggtggttc tctatgctca catctttggc tatgttcgcc agaggactat gagaatgtct   720
90 cggcatagtt ctggaccccg gcggaatcgg gataccatga tgagtcttct gaagactgtg   780
91 gtcattgtgc ttggggcctt tatcatctgc tggactcctg gattggtttt gttacttcta   840
92 gacgtgtgct gtccacagtg cgacgtgctg gcctatgaga aattcttcct tctccttgct   900
93 gaattcaact ctgccatgaa ccccatcatt tactcctacc gcgacaaaga aatgagcgcc   960
94 acctttaggc agatcctctg ctgccagcgc agtgagaacc ccaccggccc cacagaaggc  1020
95 tcagaccgct cggcttcctc cctcaaccac accatcttgg ctggagttca cagcaatgac  1080
96 cactctgtgg tt                                                     1092
98 <210> SEQ ID NO: 3
99 <211> LENGTH: 364
100 <212> TYPE: PRT
101 <213> ORGANISM: Rat
103 <400> SEQUENCE: 3
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Input Set : **A:\pto.kd.txt**
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104 Met Ala Ala Ala Ser Thr Ser Ser Pro Val Ile Ser Gln Pro Gln Phe
105                  5                  10                  15
106 Thr Ala Met Asn Glu Gln Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
107              20                  25                  30
108 Phe Tyr Asn Arg Ser Gly Lys Tyr Leu Ala Thr Glu Trp Asn Thr Val
109          35                  40                  45
110 Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Val Phe Ile Met
111      50                  55                  60
112 Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
113  65                  70                  75                  80
114 His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
115                  85                  90                  95
116 Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
117              100                 105                 110
118 Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
119          115                 120                 125
120 Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
121      130                 135                 140
122 Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
123 145                 150                 155                 160
124 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
125                 165                 170                 175
126 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
127              180                 185                 190
128 Asp His Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
129          195                 200                 205
130 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
131      210                 215                 220
132 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
133 225                 230                 235                 240
134 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
135                 245                 250                 255
136 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Val Cys Trp Thr
137              260                 265                 270
138 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
139          275                 280                 285
140 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
141      290                 295                 300
142 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
143 305                 310                 315                 320
144 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Asn Glu Asn Pro Asn Gly
145                 325                 330                 335
146 Pro Thr Glu Gly Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
147              340                 345                 350
148 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
149          355                 360
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 1092
153 <212> TYPE: DNA
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RAW SEQUENCE LISTING DATE: 06/21/2005
PATENT APPLICATION: **US/10/537,676** TIME: 13:38:24

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\06212005\J537676.raw**

154 <213> ORGANISM: Rat
156 <400> SEQUENCE: 4
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158 gaacaacagt gcttctacaa cgagtctatc gccttcttct ataaccggag tggaaagtat 120
159 ctagccacag aatggaacac tgtgagcaag ctggtgatgg gactgggcat cactgtctgc 180
160 gtgttcatca tgctggccaa tctactggtc atggtggcaa tttacgtcaa ccgccgcttc 240
161 catttcccta tttattactt gatggccaac ctggctgctg cagacttctt cgctggactg 300
162 gcctacttct acctgatgtt caacacggga cctaataccc ggagactgac cgtgagcaca 360
163 tggcttctcc ggcagggcct catcgacacc agcctgacgg cttctgtggc caacctgctg 420
164 gccattgcca tcgagaggca catcacagtt ttccgaatgc agctccatac acgaatgagc 480
165 aaccgacgtg tggtggtggt gattgtagtc atctggacta tggccattgt gatgggtgcc 540
166 atacccagtg tgggctggaa ctgcatctgt gatatcgatc attgttccaa catggcgccc 600
167 ctctacagtg actcctactt agtcttctgg gccattttca acctggtgac ctttgtggtc 660
168 atggtggttc tctacgctca catctttggc tatgttcgcc agaggactat gagaatgtcc 720
169 cggcatagtt ctggacccag gaggaatcgg gacaccatga tgagccttct gaagactgtg 780
170 gtcattgtgc tgggtgcctt tattgtctgc tggactccgg gattggtctt gctactgctc 840
171 gatgtgtgtt gcccgcagtg cgatgtcctg gcctatgaga agttcttcct cctcctggcc 900
172 gagttcaact ctgctatgaa ccccatcatc tactcctacc gcgacaaaga gatgagcgcc 960
173 accttcaggc agatcctgtg ttgccagcgc aacgagaacc ccaacggccc cacggaaggc 1020
174 tctgaccgct cggcctcctc cctcaaccac actattctgg ctggagttca cagcaatgac 1080
175 cactctgtgg tt 1092
177 <210> SEQ ID NO: 5
178 <211> LENGTH: 378
179 <212> TYPE: PRT
180 <213> ORGANISM: human
182 <400> SEQUENCE: 5
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184 5 10 15
185 Thr Leu Arg Glu His Tyr Gln Tyr Val Gly Lys Leu Ala Gly Arg Leu
186 20 25 30
187 Lys Glu Ala Ser Glu Gly Ser Thr Leu Thr Thr Val Leu Phe Leu Val
188 35 40 45
189 Ile Cys Ser Phe Ile Val Leu Glu Asn Leu Met Val Leu Ile Ala Ile
190 50 55 60
191 Trp Lys Asn Asn Lys Phe His Asn Arg Met Tyr Phe Phe Ile Gly Asn
192 65 70 75 80
193 Leu Ala Leu Cys Asp Leu Leu Ala Gly Ile Ala Tyr Lys Val Asn Ile
194 85 90 95
195 Leu Met Ser Gly Lys Lys Thr Phe Ser Leu Ser Pro Thr Val Trp Phe
196 100 105 110
197 Leu Arg Glu Gly Ser Met Phe Val Ala Leu Gly Ala Ser Thr Cys Ser
198 115 120 125
199 Leu Leu Ala Ile Ala Ile Glu Arg His Leu Thr Met Ile Lys Met Arg
200 130 135 140
201 Pro Tyr Asp Ala Asn Lys Arg His Arg Val Phe Leu Leu Ile Gly Met
202 145 150 155 160
203 Cys Trp Leu Ile Ala Phe Thr Leu Gly Ala Leu Pro Ile Leu Gly Trp
204 165 170 175
205 Asn Cys Leu His Asn Leu Pro Asp Cys Ser Thr Ile Leu Pro Leu Tyr

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Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\06212005\J537676.raw

```
206             180                 185                 190
207 Ser Lys Lys Tyr Ile Ala Phe Cys Ile Ser Ile Phe Thr Ala Ile Leu
208         195                 200                 205
209 Val Thr Ile Val Ile Leu Tyr Ala Arg Ile Tyr Phe Leu Val Lys Ser
210     210                 215                 220
211 Ser Ser Arg Lys Val Ala Asn His Asn Asn Ser Glu Arg Ser Met Ala
212 225                 230                 235                 240
213 Leu Leu Arg Thr Val Val Ile Val Val Ser Val Phe Ile Ala Cys Trp
214                 245                 250                 255
215 Ser Pro Leu Phe Ile Leu Phe Leu Ile Asp Val Ala Cys Arg Val Gln
216             260                 265                 270
217 Ala Cys Pro Ile Leu Phe Lys Ala Gln Trp Phe Ile Val Leu Ala Val
218         275                 280                 285
219 Leu Asn Ser Ala Met Asn Pro Val Ile Tyr Thr Leu Ala Ser Lys Glu
220     290                 295                 300
221 Met Arg Arg Ala Phe Phe Arg Leu Val Cys Asn Cys Leu Val Arg Gly
222 305                 310                 315                 320
223 Arg Gly Ala Arg Ala Ser Pro Ile Gln Pro Ala Leu Asp Pro Ser Arg
224                 325                 330                 335
225 Ser Lys Ser Ser Ser Ser Asn Asn Ser Ser His Ser Pro Lys Val Lys
226             340                 345                 350
227 Glu Asp Leu Pro His Thr Asp Pro Ser Ser Cys Ile Met Asp Lys Asn
228         355                 360                 365
229 Ala Ala Leu Gln Asn Gly Ile Phe Cys Asn
230     370                 375
232 <210> SEQ ID NO: 6
233 <211> LENGTH: 1134
234 <212> TYPE: DNA
235 <213> ORGANISM: human
237 <400> SEQUENCE: 6
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239 cattaccagt acgtggggaa gttggcgggc aggctgaagg aggcctccga gggcagcacg   120
240 ctcaccaccg tgctcttctt ggtcatctgc agcttcatcg tcttggagaa cctgatggtt   180
241 ttgattgcca tctggaaaaa caataaattt cacaaccgca tgtacttttt cattggcaac   240
242 ctggctctct gcgacctgct ggccggcatc gcttacaagg tcaacattct gatgtctggc   300
243 aagaagacgt tcagcctgtc tcccacggtc tggttcctca gggagggcag tatgttcgtg   360
244 gcccttgggg cgtccacctg cagcttactg gccatcgcca tcgagcggca cttgacaatg   420
245 atcaaaatga ggccttacga cgccaacaag aggcaccgcg tcttcctcct gatcgggatg   480
246 tgctggctca ttgccttcac gctgggcgcc ctgcccattc tgggctggaa ctgcctgcac   540
247 aatctccctg actgctctac catcctgccc ctctactcca agaagtacat tgccttctgc   600
248 atcagcatct tcacggccat cctggtgacc atcgtgatcc tctacgcacg catctacttc   660
249 ctggtgaagt ccagcagccg taaggtggcc aaccacaaca actcggagcg gtccatggca   720
250 ctgctgcgga ccgtggtgat tgtggtgagc gtgttcatcg cctgctggtc cccactcttc   780
251 atcctcttcc tcattgatgt ggcctgcagg gtgcaggcgt gccccatcct cttcaaggct   840
252 cagtggttca tcgtgttggc tgtgctcaac tccgccatga acccggtcat ctacacgctg   900
253 gccagcaagg agatgcggcg ggccttcttc cgtctggtct gcaactgcct ggtcagggga   960
254 cgggggccc gcgcctcacc catccagcct gcgctcgacc caagcagaag taaatcaagc  1020
255 agcagcaaca atagcagcca ctctccgaag gtcaaggaag acctgcccca cacagacccc  1080
256 tcatcctgca tcatggacaa gaacgcagca cttcagaatg ggatcttctg caac        1134
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VERIFICATION SUMMARY DATE: 06/21/2005
PATENT APPLICATION: **US/10/537,676** TIME: 13:38:25

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\06212005\J537676.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date